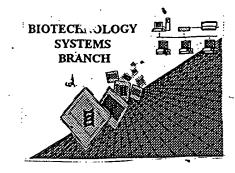UCAC
0400

BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: ___10|005,337___

Source: ___OIPE___

Date Processed by STIC: ___12|14|01___)

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10|005,337

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
_____ Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 _____ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
_____ Numbering use space characters, instead.

4 _____ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
_____ "bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
_____ (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
_____ (NEW RULES) <210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
_____ (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
_____ Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 ✓ Use of <220> Sequence(s) 4 +5 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
_____ "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

OIPE

RAW SEQUENCE LISTING   DATE: 12/14/2001
PATENT APPLICATION: US/10/005,337   TIME: 09:51:23

Input Set : A:\Seqlist6064.txt   Does Not Comply
Output Set: N:\CRF3\12142001\I005337.raw   Corrected Diskette Needed

```
    3 <110> APPLICANT: BENOIT, Patrick
    4        SCHWARTZ, Bertrand
    5        BRANELLEC, Didier
    6        CHIEN, Kenneth R.
    8 <120> TITLE OF INVENTION: SEQUENCES UPSTREAM OF THE CARP GENE, VECTORS CONTAINING
    9        THEM AND USES THEREOF
   11 <130> FILE REFERENCE: 03806.0530-00000
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/005,337
   15 <141> CURRENT FILING DATE: 2001-12-07
   17 <160> NUMBER OF SEQ ID NOS: 5
   19 <170> SOFTWARE: PatentIn Ver. 2.1
   21 <210> SEQ ID NO: 1
   22 <211> LENGTH: 2358
   23 <212> TYPE: DNA
   24 <213> ORGANISM: Mus musculus
   26 <400> SEQUENCE: 1
   27 ggatcctttc atgtttaaca atatcaaccc taacccaagg ggaacagcct gcctgacagt 60
   28 ggctttgcca cccatgaata cttcctagtc tagtccgttt gtgaaactca gcccatccca 120
   29 acacttctgc aagccccatc ctctacaagg tgctcattgg gaatttcctg gagcttctct 180
   30 ttcaggatca gcctgattct agggcagcag ttctcaacct gggggcctcg accccatttgg 240
   31 gggaatcaaa cgacccttta caggggtcac atatcatcta tcctatatgt caggtattta 300
   32 cattacgatt cgtaacagta gcaaaattac aggtatgaaa tagcaatgaa ataattttat 360
   33 gattgaaggt caccacaaca tgaggccgcc acactgttct agagaaaaat cacctgggtg 420
   34 gggaaaggtt tgggaaagcc tttctgtcca ttcttcattc ttcaaagtga tgtgttcaca 480
   35 gaaagccttt cagctgttct gctggggctc ttagtaagtc tgagtaggaa ctgtatgtac 540
   36 caggtctgct tcttatgggt ggagccaaga cgcatcgtgg gtggagcgaa gacgcaacct 600
   37 caccttctag ctctgcatcc atagcaagta gcctaatgtt tctgtgtcta ggtgtcatct 660
   38 ctgtgaatcg agatccttgg ccttgcttga attagggagg cacaaaatac tcagagattc 720
   39 aagactgctc agcagcccag agtccttcct caaaggaaag gtctcaactc tcagcccccc 780
   40 ttagctctga gtcaggcctg gaacaaacgg ccacaggaat gagaaaagct gccatagctg 840
   41 cttgtcactt caagaggtca aagaaaatag tgttaaccat gaaaacgaga agaccaacag 900
   42 ttatccattg atagcgtctc aggacagata ggacagagag aacactagga gaggggaacc 960
   43 cacgaaggac aaggtattag tgtgttggtt ttcagggcaa tgtcttgtac tgaagattct 1020
   44 agaaacacaa tttgctggtt gaacagctga agtggggtgg gggttcttac cccatgttca 1080
   45 tggaagggtg agtgaggaga gacagatata tgatggccag cataacaaac atacacaaca 1140
   46 ccctaattaa cacttccctc ttctactgac accccttca ctctcctctt tcataaaaaa 1200
   47 taaaaaaagt atttttatgtg gctcttacga tagaatcttt cctcgaacta taaaaagatc 1260
   48 taaatattta tatttttcac attttaatat cttagcgatg acaagccaga aacaagtatt 1320
   49 ttttgcctct ctcaacagca aagcttgggg ccttttttgtt tccgtgttag gaatagaaca 1380
   50 cgagagcccc gtgtatctag gcagatgctc tatcattagc ccatgagtct ccagcctcag 1440
   51 acgcacattt ttctcgggct ctcttaagct tttcccacag cattgggaaa ctttactgac 1500
   52 agcatccaag ttgtgcttct gctaagaact ggactacat ctctctgtgc atcacttcgg 1560
   53 cccgtttttgg ggtagatcct ctgattagcc ttcagattta gaacacggtg agcctgtggt 1620
   54 gcactaatta tggccagtga caccatagag tcaaagtgca ttactgaatg ctttcaattt 1680
   55 ctcctaatgc tggtacgatg gcatgtcaca gggccatttt agctgcagac atcactccag 1740
   56 agaattccaa acagatagag acaagtggca cccagaccca tctccttccc ctcgggctga 1800
   57 ttatccccag aaataggatg tcccaaagca acacttccca gccaactgga gtgctgataa 1860
```

RAW SEQUENCE LISTING   DATE: 12/14/2001
PATENT APPLICATION: US/10/005,337   TIME: 09:51:23

Input Set : **A:\Seqlist6064.txt**
Output Set: **N:\CRF3\12142001\I005337.raw**

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58 gtccagttat cagaaagata tggctgtaag tgtgatgcac agtgcttgca ttttcttgat 1920
59 acgttagtca tatgagagct gacaaagaag gaaaaagagc agcgatgtgg tgcaatatta 1980
60 acaggcagct gtcccctggc ttcccgatac gtgggatgac tcgcattgct gagcggtgtg 2040
61 gtcactgcca aaggaatgac cctctcacat ttcttcctga ttcgcatacg ccgcggccag 2100
62 cttgtcatct ccctcttggg cttcccagac actaagtctg gaatgaaaat tcacctgcct 2160
63 ctgaattggc cactggtggg ggcaggggtg tgacttggct tcccaggctg gaagattatc 2220
64 tcacccagcc ctagctatat aacgggctgg tgtggagggg ctccacaggg ccagttccag 2280
65 gggttcatcc acaagagaga aaaacataga ctcgaggtct agggagcttg catgcctgca 2340
66 ggtcggaggc caccatgg                                               2358
69 <210> SEQ ID NO: 2
70 <211> LENGTH: 2074
71 <212> TYPE: DNA
72 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 2
75 ctgcagcaag ttacttaatg ttttttgcct cagcatcctc tctgtaaaat gagagcatta 60
76 gtcttgctcc aacttcgagg gcatggacag ctctgggatt tcatatccaa gacccttaaa 120
77 catcccacag tccttccccc aaacacttct cctcctaata cctccctcag tttgggtcag 180
78 gcctggaaca aaaaggcata cgaaatggta gaaaaagtgt ccatgactac ttctgactta 240
79 gatgaagaga ccaatgaaaa tagtaatgac tctgtttgct tcagcaggac atatactaaa 300
80 ataggagcta tacaaagaag attagcatgg actctgtgca agaatgacac acaaatttgt 360
81 gaaacattcc atatattaaa aataaataaa taataaagag aaaaggaaaa aattaaaaag 420
82 aaaatagtga tagctgtgtc catctcaaag aaaagcccag gagatttcct ttatttaccc 480
83 cctttaagat agaatattag gagaccggaa catatgatac aggaggtact gggagggtcc 540
84 ctctttgtca atgttttgtc ttggggtggg gagtcgatgt cttctcaaag tttcagaaac 600
85 accatccact gactgagcat tcaaggggca agaggagaat ggcagccaca tttgttgatt 660
86 gggtgagttt ggggagaaat agacacacaa aggtcaaaca taacttccta attaacactt 720
87 ccctccattc acaattccct tctcccattc ttctctcctg tcttttacts akaraaaccc 780
88 agttttcct gaaactataa aaatacccc agtatgttta cataatttac acctcaaaga 840
89 ttagaaacca gaaatagaga ccttttcaac ccttccggaa gcaaagtgca ttatccctcc 900
90 agccacgtgt ctcaaatctt gatgcatcag aatcatctgg gtgctttkaa attcaagatg 960
91 attcctacga gttaccataa atcaactcag aattccctgg agtggggcca gggatctgta 1020
92 tttctgacaa gctcccacag gtgattcctt tccccacagc atttgagaac ttcagctcaa 1080
93 tgacctaatc agagtcctgc cattgctaat atctggtctc atttttbtca tatatatata 1140
94 tagtatttgt ggtagagatg ggattttgcc atgttgccca ggctagtatt gaactcctaa 1200
95 gctaagcaat cttcctgtct ctgcctccca aaatgttggg attacaggtg taagccactg 1260
96 cacccggctg atagctggtt tcatttactc tatttcttga ccactctgat ccattttgaa 1320
97 gtaaaaatgc tccaattatt atgctgtttt agaacacggt aagcatgtca tgtgctaatg 1380
98 gccagtgaca tcataaaaga aaagtgcatt actgaatgct ttcaatgtct tataatgatg 1440
99 gtaaggtggc atgtcatggg gcctatttag cccagacatc actccaaaga attccaaaca 1500
100 gatatagaca agtgccttta gggcccagat cccttcccct caggctgttt acccagggaa 1560
101 taggatgtcc tgggacaagt ttcccctaag tgaagtgttg ataagtctgc ttatcagaaa 1620
102 gatattactg ggggtgtgat atgtagggca tctacatttt cttgataggt agtcatatga 1680
103 aagctgacaa agaaaaaaag ggcagtgatg tggtgcaatg tcaacagaca gctgtcccct 1740
104 gactcttgac aaataggatg acttgcattg ctgagcgatg tgatcaccac caaaggaatg 1800
105 gccctctcac atttcttcct gattcacata ttcagcaggg ttagcttgtc ctcccctccc 1860
106 tcttcagctt cccagacact gagtctggaa tgaaaattca cctgcctctg agttggctcc 1920
107 taatggggc gggagtgtta cttcggttcc caggttggaa gattatctca cccggcccca 1980
108 gctatataag ctgaccggtg tggaggggcc cagcagggcc aactccaggg attccttcca 2040
109 cgacagaaaa acatacaaga ctccttcagc caac                            2074
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/005,337

DATE: 12/14/2001
TIME: 09:51:23

Input Set : A:\Seqlist6064.txt
Output Set: N:\CRF3\12142001\I005337.raw

```
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 750
114 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens
117 <400> SEQUENCE: 3
118 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
119   1               5                  10                  15
121 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
122              20                  25                  30
124 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
125              35                  40                  45
127 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
128          50                  55                  60
130 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
131  65                  70                  75                  80
133 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
134              85                  90                  95
136 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
137              100                 105                 110
139 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
140              115                 120                 125
142 Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
143          130                 135                 140
145 Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
146 145                 150                 155                 160
148 Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
149              165                 170                 175
151 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
152              180                 185                 190
154 Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
155              195                 200                 205
157 Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
158          210                 215                 220
160 Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
161 225                 230                 235                 240
163 Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu
164              245                 250                 255
166 Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys
167              260                 265                 270
169 Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp
170              275                 280                 285
172 Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu
173          290                 295                 300
175 Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala
176 305                 310                 315                 320
178 Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn
179              325                 330                 335
181 Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
182              340                 345                 350
```

file://C:\Crf3\Outhold\VsrI005337.htm

12/14/01

RAW SEQUENCE LISTING   DATE: 12/14/2001
PATENT APPLICATION: US/10/005,337   TIME: 09:51:23

Input Set : A:\Seqlist6064.txt
Output Set: N:\CRF3\12142001\I005337.raw

```
184 Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu
185         355             360             365
187 Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu
188         370             375             380
190 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
191 385             390             395             400
193 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
194             405             410             415
196 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
197             420             425             430
199 Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
200         435             440             445
202 Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu
203         450             455             460
205 Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
206 465             470             475             480
208 Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
209             485             490             495
211 Leu Gln Glu Ile Tyr Lys Asp Leu Tyr Ala Trp Ala Ile Leu Thr Gly
212             500             505             510
214 Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu
215         515             520             525
217 Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln
218         530             535             540
220 Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe
221 545             550             555             560
223 Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile
224             565             570             575
226 Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys
227             580             585             590
229 Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn
230             595             600             605
232 Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu
233         610             615             620
235 Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys
236 625             630             635             640
238 Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp
239             645             650             655
241 Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly
242             660             665             670
244 Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln
245         675             680             685
247 Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu
248         690             695             700
250 Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr
251 705             710             715             720
253 Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met
254             725             730             735
256 Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
```

```
                    RAW SEQUENCE LISTING            DATE: 12/14/2001
                    PATENT APPLICATION:  US/10/005,337    TIME: 09:51:23

                    Input Set : A:\Seqlist6064.txt
                    Output Set: N:\CRF3\12142001\I005337.raw

        257             740             745             750
        260 <210> SEQ ID NO: 4
        261 <211> LENGTH: 30
        262 <212> TYPE: DNA
        263 <213> ORGANISM: Artificial sequence
W--> 265 <220> FEATURE:
W--> 265 <223> OTHER INFORMATION:
        265 <400> SEQUENCE: 4
C--> 266 ggcgatttaa ataatgtagt cttatgcaat                              30
        269 <210> SEQ ID NO: 5
        270 <211> LENGTH: 31
        271 <212> TYPE: DNA
        272 <213> ORGANISM: Artificial sequence
W--> 274 <220> FEATURE:
W--> 274 <223> OTHER INFORMATION:
        274 <400> SEQUENCE: 5
C--> 275 ggggtctaga aggtgcacac caatgtggtg a                           31
```

Requires ∠2207 to ∠2237 — with explanation for Artificial Sequence; see error summary sheet item 11

VERIFICATION SUMMARY　　　　　　　　　DATE: 12/14/2001
PATENT APPLICATION:　US/10/005,337　　　TIME: 09:51:24

Input Set : **A:\Seqlist6064.txt**
Output Set: **N:\CRF3\12142001\I005337.raw**

```
L:13  M:270 C: Current Application Number differs, Replaced Application Number
L:265 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:265 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:266 M:112 C: (48) String data converted to lower case,
L:274 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:274 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:275 M:112 C: (48) String data converted to lower case,
```